AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions, and listings of claims in the application.

Listing of claims

1. (Currently amended) A method for of identifying ~~an individual who has~~ a human having an altered risk for developing ~~an autoimmune disease~~ Rheumatoid Arthritis (RA), comprising detecting the presence of a single nucleotide polymorphism (SNP) ~~as represented by a nucleotide sequence selected from the group consisting~~ at position 101 of SEQ ID ~~NOs~~ NO: 5502~~, 3379, 4292, 5446, 4758, and 4914~~ or its complement thereof in said ~~individual's~~ human's nucleic acids, wherein the presence of the SNP is ~~correlated with~~ indicative of an altered risk for ~~autoimmune disease~~ developing RA in said human.

2. - 26. (Canceled)

27. (New) The method of claim 1 in which said human is positive for rheumatoid factor (RF+).

28. (New) The method of claim 1 in which said human is negative for rheumatoid factor (RF-).

29. (New) The method of claim 1 in which SEQ ID NO: 5502 is contained within the genomic sequence of TRIP gene as represented by SEQ ID NO: 1688.

30. (New) The method of claim 1 in which the SNP to be detected is located at position 6497 of SEQ ID NO: 1688.

31. (New) The method of claim 1 in which said human's nucleic acids are extracted from a biological sample therefrom.

32. (New) The method of claim 28 in which said biological sample is blood.

33. (New) The method of claim 1 in which said human's nucleic acids are amplified before the detection is carried out.

34. (New) The method of claim 1 in which detection is carried out by using detection reagents comprising the nucleotide sequences of SEQ ID NO: 6629, SEQ ID NO: 6630, and SEQ ID NO: 6631.

35. (New) The method of claim 1 in which detection is carried out by a process selected from the group consisting of: allele-specific probe hybridization, allele-specific primer extension, allele-specific amplification, sequencing, 5' nuclease digestion, molecular beacon assay, oligonucleotide ligation assay, size analysis, and single-stranded conformation polymorphism.

36. (New) A method of identifying a human having an increased risk for developing Rheumatoid Arthritis (RA), comprising detecting the presence of a single nucleotide polymorphism (SNP) at position 101 of SEQ ID NO: 5502 or its complement thereof in said human's nucleic acids, wherein the presence of the SNP is indicative of an increased risk for developing RA in said human.

37. (New) The method of claim 36 in which said human is positive for rheumatoid factor (RF+).

38. (New) The method of claim 36 in which said human is negative for rheumatoid factor (RF-).

39. (New) The method of claim 36 in which SEQ ID NO: 5502 is contained within the genomic sequence of TRIP gene as represented by SEQ ID NO: 1688.

40. (New) The method of claim 36 in which the SNP to be detected is located at position 6497 of SEQ ID NO: 1688.

41. (New) The method of claim 36 in which said human's nucleic acids are extracted from a biological sample therefrom.

42. (New) The method of claim 41 in which said biological sample is blood.

43. (New) The method of claim 36 in which said human's nucleic acids are amplified before the detection is carried out.

44. (New) The method of claim 36 in which detection is carried out by using detection reagents comprising the nucleotide sequences of SEQ ID NO: 6629, SEQ ID NO: 6630, and SEQ ID NO: 6631.

45. (New) The method of claim 36 in which detection is carried out by a process selected from the group consisting of: allele-specific probe hybridization, allele-specific primer extension, allele-specific amplification, sequencing, 5' nuclease digestion, molecular beacon assay, oligonucleotide ligation assay, size analysis, and single-stranded conformation polymorphism.

46. (New) A method of identifying a human having a decreased risk for developing myocardial infarction, comprising detecting the presence of a single nucleotide polymorphism (SNP) at position 101 of SEQ ID NO: 5502 or its complement thereof in said human's nucleic acids, wherein the presence of T at position 101 of SEQ ID NO: 5502 is indicative of a decreased risk for myocardial infarction in said human.

47. (New) The method of claim 46 in which said human is positive for rheumatoid factor (RF+).

48. (New) The method of claim 46 in which said human is negative for rheumatoid factor (RF-).

49. (New) The method of claim 46 in which SEQ ID NO: 5502 is contained within the genomic sequence of TRIP gene as represented by SEQ ID NO: 1688.

50. (New) The method of claim 46 in which the SNP to be detected is located at position 6497 of SEQ ID NO: 1688.

51. (New) The method of claim 46 in which said human's nucleic acids are extracted from a biological sample therefrom.

52. (New) The method of claim 51 in which said biological sample is blood.

53. (New) The method of claim 46 in which said human's nucleic acids are amplified before the detection is carried out.

54. (New) The method of claim 46 in which detection is carried out by using detection reagents comprising the nucleotide sequences of SEQ ID NO: 6629, SEQ ID NO: 6630, and SEQ ID NO: 6631.

55. (New) The method of claim 46 in which detection is carried out by a process selected from the group consisting of: allele-specific probe hybridization, allele-specific primer extension, allele-specific amplification, sequencing, 5' nuclease digestion, molecular beacon assay, oligonucleotide ligation assay, size analysis, and single-stranded conformation polymorphism.

56. (New) A method of determining a human's risk for developing RA, comprising detecting a single nucleotide polymorphism (SNP) at position 101 of SEQ ID NO: 5502 or its complement thereof in said human's nucleic acids, wherein the presence of C at position 101 of SEQ ID NO: 5502 is indicative of an increased risk for RA in said human, or, the presence of T at position 101 of SEQ ID NO: 5502 is indicative of a decreased risk for developing RA in said human.

57. (New) The method of claim 56 in which said human is positive for rheumatoid factor (RF+).

58. (New) The method of claim 56 in which said human is negative for rheumatoid factor (RF-).

59. (New) The method of claim 56 in which SEQ ID NO: 5502 is contained within the genomic sequence of TRIP gene as represented by SEQ ID NO: 1688.

60. (New) The method of claim 56 in which the SNP to be detected is located at position 6497 of SEQ ID NO: 1688.

61. (New) The method of claim 56 in which said human's nucleic acids are extracted from a biological sample therefrom.

62. (New) The method of claim 61 in which said biological sample is blood.

63. (New) The method of claim 56 in which said human's nucleic acids are amplified before the detection is carried out.

64. (New) The method of claim 56 in which detection is carried out by using detection reagents comprising the nucleotide sequences of SEQ ID NO: 6629, SEQ ID NO: 6630, and SEQ ID NO: 6631.

65. (New) The method of claim 56 in which detection is carried out by a process selected from the group consisting of: allele-specific probe hybridization, allele-specific primer extension, allele-specific amplification, sequencing, 5' nuclease digestion, molecular beacon assay, oligonucleotide ligation assay, size analysis, and single-stranded conformation polymorphism.